

# SEQUENCE LISTING

<110> Wood, Clive  
Chaudhary, Divya  
Long, Andrew

<120> TRADE MOLECULES, AND USES RELATED THERE TO

<130> GNN-012CP

<140>

<141>

<150> 60/181,922

<151> 2000-02-11

<150> 60/182,148

<151> 2000-02-14

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1251)

<400> 1

atg gct tta aaa gtg cta cta gaa caa gag aaa acg ttt ttc act ctt	48
Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu	
01 5 10 15	
tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa tca gga	96
Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly	
20 25 30	
gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc	144
Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro	
35 40 45	
tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc	192
Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50 55 60	
ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc	240
Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe	
65 70 75 80	
aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca	288
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala	
85 90 95	

gtg	gtg	aac	cgc	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	336
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
		100						105					110			
atc	tgc	ggg	gac	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	384
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
		115					120					125				
ggc	ttt	caa	gac	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	432
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130					135					140					
tac	gaa	ccg	cac	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	480
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
acg	gcc	tcc	agc	cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	528
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
gct	ctg	gcc	acc	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	576
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
tgt	aag	aga	cag	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	624
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
gag	gac	att	cag	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ttt	gac	aga	cct	672
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	
	210					215					220					
gag	ctc	cac	gaa	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	720
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
tca	gtg	cag	acc	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	768
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
gag	gag	gcc	tgc	agc	ccc	aac	ccg	gcg	act	ctt	ggt	tgt	ggg	gtg	cat	816
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
		260						265					270			
tct	gca	gcc	agt	ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	864
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
gtg	ccg	act	ttc	ttc	gga	tcc	ctc	acg	cag	tcc	atc	tgt	ggc	gag	ttt	912
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
tca	gat	gcc	tgg	cct	ctg	atg	cag	aat	ccc	atg	ggt	ggt	gac	aac	atc	960
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310				315						320	
tct	ttt	tgt	gac	tct	tat	cct	gaa	ctc	act	gga	gaa	gac	att	cat	tct	1008

Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser		
				325					330					335			
ctc	aat	cca	gaa	ctt	gaa	agc	tca	acg	tct	ttg	gat	tca	aat	agc	agt	1056	
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser		
			340					345					350				
caa	gat	ttg	gtt	ggg	gct	gtt	cca	gtc	cag	tct	cat	tct	gaa	aac	1104		
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn		
			355				360					365					
ttt	aca	gca	gct	act	gat	tta	tct	aga	tat	aac	aac	aca	ctg	gta	gaa	1152	
Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu		
	370					375					380						
tca	gca	tca	act	cag	gat	gca	cta	act	atg	aga	agc	cag	cta	gat	cag	1200	
Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln		
385					390					395				400			
gag	agt	ggc	gct	atc	atc	cac	cca	gcc	act	cag	acg	tcc	ctc	cag	gaa	1248	
Glu	Ser	Gly	Ala	Ile	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Glu		
				405				410					415				
gct	taa	gaa	ac	ct	gct	tct	tct	tct	gc	agt	aga	ag	cgt	gt	gct	gg	aacccaaaga
Ala																	1301
gact	cctt	g	tt	agg	ctta	t	gg	act	gag	c	agt	ct	gg	acc	tt	gcat	ggct
																	tctggggcaa
																	1361
aat	gaat	ct	ga	ac	caa	act	gac	gg	catt	tt	ga	gc	ctt	tc	ag	cc	agttgc
																	ttctgagcca
																	1421
gacc	agct	gt	aag	ct	gaa	ac	ct	caat	gaat	aaca	ag	aaaa	gact	cc	ag	gc	cgactcatga
																	1481
tact	ct	gcat	ttt	ct	taca	t	gaga	ag	ctt	ct	tg	cc	aca	aa	ag	t	gactt
																	caaagacgga
																	1541
gggt	t	gag	c	gc	cta	t	gag	att	gtg	gac	at	ata	aac	aaga	aa	caga	aatgccctca
																	1601
gctt	at	ttt	cat	gg	t	gatt	gt	gg	ttt	tac	aag	act	ga	ag	acc	cag	agta
																	tactttttc
																	1660

<210> 2  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

Met	Ala	Leu	Lys	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu		
1				5					10					15			
Leu	Val	Leu	Leu	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Ser	Gly		
				20				25					30				
Asp	Cys	Arg	Gln	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro		
		35					40					45					
Cys	Asn	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe		
	50					55					60						

Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	65	70	75	80
Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	85	90	95	
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	100	105	110	
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	115	120	125	
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	130	135	140	
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	145	150	155	160
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	165	170	175	
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	180	185	190	
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	195	200	205	
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	210	215	220	
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	225	230	235	240
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	245	250	255	
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	260	265	270	
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	275	280	285	
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	290	295	300	
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	305	310	315	320
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser	325	330	335	
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	340	345	350	
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	355	360	365	

Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu  
 370 375 380

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln  
 385 390 395 400

Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu  
 405 410 415

Ala

<210> 3  
 <211> 1325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1269)

<400> 3  
 atg gct tta aaa gtg cta cta gaa caa gag aaa acg ttt ttc act ctt 48  
 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu  
 5 10 15

tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga 96  
 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly  
 20 25 30

gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc 144  
 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro  
 35 40 45

gac aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc 192  
 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
 50 55 60

ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc 240  
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe  
 65 70 75 80

aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca 288  
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala  
 85 90 95

gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc 336  
 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala  
 100 105 110

atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc 384  
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
 115 120 125

ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct cct 432  
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro

130	135	140	
tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser 145 150 155 160			480
acg gcc tcc agc cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser 165 170 175			528
gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr 180 185 190			576
tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser 195 200 205			624
cag gac att cag tac aac ggc tct gag ctg tcg tgt ctt gac aga cct Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro 210 215 220			672
cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp 225 230 235 240			720
tca gtg cag acc tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys 245 250 255			768
gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His 260 265 270			816
tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met 275 280 285			864
gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe 290 295 300			912
tca gat gcc tgg cct ctg atg cag aat ccc atg ggt ggt gac aac atc Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile 305 310 315 320			960
tct ttt tgt gac tct tat cct gaa ctc gct gga gaa gac att cat tct Ser Phe Cys Asp Ser Tyr Pro Glu Leu Ala Gly Glu Asp Ile His Ser 325 330 335			1008
ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser 340 345 350			1056
caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn 355 360 365			1104

ttt	aca	gca	gct	act	gat	tta	tct	aga	tat	aac	aac	aca	ctg	gta	gaa	1152
Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu	
	370					375					380					

tca	gca	tca	act	cag	gat	gca	cta	act	atg	aga	agc	cag	cta	gat	cag	1200
Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln	
	385				390					395					400	

gag	agt	ggc	gct	atc	atc	cac	cca	gcc	act	cag	acg	tcc	ctc	cag	gta	1248
Glu	Ser	Gly	Ala	Ile	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Val	
				405					410					415		

agg	cag	cga	ctg	ggg	tcc	ctg	tgaacacagc	actgacttac	agtagatcag							1299
Arg	Gln	Arg	Leu	Gly	Ser	Leu										
				420												

aactctgttc	ccagcataag	atttgg														1325
------------	------------	--------	--	--	--	--	--	--	--	--	--	--	--	--	--	------

<210> 4  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

Met	Ala	Leu	Lys	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu	
1				5					10					15		
Leu	Val	Leu	Leu	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Thr	Gly	
				20				25					30			
Asp	Cys	Arg	Gln	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro	
		35					40					45				
Cys	Asn	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	
	50					55					60					
Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	
65					70					75					80	
Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
				85					90					95		
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
		100						105					110			
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
		115					120					125				
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130					135					140					
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	

165							170						175			
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	
	210					215					220					
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230					235					240	
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Ala	Gly	Glu	Asp	Ile	His	Ser	
				325					330					335		
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	
			340					345					350			
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	
		355					360					365				
Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu	
	370					375					380					
Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln	
385					390					395					400	
Glu	Ser	Gly	Ala	Ile	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Val	
				405					410					415		
Arg	Gln	Arg	Leu	Gly	Ser	Leu										
			420													

<210> 5  
 <211> 1914  
 <212> DNA  
 <213> Mus musculus

<220>



<221> CDS

<222> (1)..(1248)

<400> 5

atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc	48
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala	
1 5 10 15	
att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga	96
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly	
20 25 30	
gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc	144
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu	
35 40 45	
tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc	192
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50 55 60	
ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc	240
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe	
65 70 75 80	
aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg	288
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala	
85 90 95	
gtg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct	336
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala	
100 105 110	
tgc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt	384
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
115 120 125	
ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc	432
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro	
130 135 140	
tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc	480
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser	
145 150 155 160	
acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt	528
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser	
165 170 175	
gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac	576
Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr	
180 185 190	
tgc aag agg cag ttc atg gag aag aaa ccc agc tgg tct ctg cgg tca	624
Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser	
195 200 205	
cag gac att cag tac aat ggc tct gag ctg tca tgc ttt gac cag cct	672

Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Gln	Pro		
210						215					220						
cgg	ctc	cgc	cac	tgt	gcc	cat	aga	gca	tgc	tgt	cag	tat	cac	cgg	gac	720	
Arg	Leu	Arg	His	Cys	Ala	His	Arg	Ala	Cys	Cys	Gln	Tyr	His	Arg	Asp		
225					230					235					240		
tca	gcc	cca	atg	tat	ggg	cct	gtt	cac	ctg	att	ccg	tcc	ttg	tgc	tgt	768	
Ser	Ala	Pro	Met	Tyr	Gly	Pro	Val	His	Leu	Ile	Pro	Ser	Leu	Cys	Cys		
				245					250					255			
gaa	gag	gcc	cgc	agc	tct	gcc	cga	gct	gtg	ctt	ggc	tgt	ggg	ctg	cgt	816	
Glu	Glu	Ala	Arg	Ser	Ser	Ala	Arg	Ala	Val	Leu	Gly	Cys	Gly	Leu	Arg		
			260					265					270				
tct	ccc	act	acc	ctc	cag	gag	aga	aac	ccg	gct	tct	gtg	ggg	gac	acg	864	
Ser	Pro	Thr	Thr	Leu	Gln	Glu	Arg	Asn	Pro	Ala	Ser	Val	Gly	Asp	Thr		
		275					280					285					
atg	cca	gcc	ttc	ttc	ggg	tct	gtt	tcc	cgt	tcc	atc	tgc	gct	gaa	ttt	912	
Met	Pro	Ala	Phe	Phe	Gly	Ser	Val	Ser	Arg	Ser	Ile	Cys	Ala	Glu	Phe		
		290				295					300						
tct	gat	gcc	tgg	cct	ctg	atg	cag	aat	cct	ctg	ggg	ggg	gac	agc	tct	960	
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Leu	Gly	Gly	Asp	Ser	Ser		
					310					315					320		
cgc	tgt	gac	tct	tat	cct	gaa	ctc	act	gga	gaa	gat	acc	aat	tcc	ctc	1008	
Leu	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Thr	Asn	Ser	Leu		
				325					330					335			
aat	ccc	gaa	aac	gaa	agc	gca	gca	tct	ctg	gat	tcc	agt	ggc	ggc	cag	1056	
Asn	Pro	Glu	Asn	Glu	Ser	Ala	Ala	Ser	Leu	Asp	Ser	Ser	Gly	Gly	Gln		
			340					345					350				
gat	ctg	gct	ggg	aca	gct	gct	cta	gag	tct	tct	ggg	aat	gtt	tca	gaa	1104	
Asp	Leu	Ala	Gly	Thr	Ala	Ala	Leu	Glu	Ser	Ser	Gly	Asn	Val	Ser	Glu		
			355				360					365					
tct	act	gac	tca	cct	aga	cat	ggg	gac	act	ggg	aca	gtc	tgg	gag	cag	1152	
Ser	Thr	Asp	Ser	Pro	Arg	His	Gly	Asp	Thr	Gly	Thr	Val	Trp	Glu	Gln		
		370				375					380						
acg	cta	gct	cag	gat	gct	caa	agg	act	cca	agc	caa	gga	ggc	tgg	gaa	1200	
Thr	Leu	Ala	Gln	Asp	Ala	Gln	Arg	Thr	Pro	Ser	Gln	Gly	Gly	Trp	Glu		
				390						395					400		
gac	agg	gaa	aac	ctg	aat	cta	gcc	atg	ccc	aca	gcc	ttc	cag	gat	gcc	1248	
Asp	Arg	Glu	Asn	Leu	Asn	Leu	Ala	Met	Pro	Thr	Ala	Phe	Gln	Asp	Ala		
			405					410					415				
tgaaggccat	cttcctgacg	tggaggtgtg	gggtctggaca	agcctgtgat	gaggcctaca	1308											
gactgagcag	tcttggtgtc	tggaagcaaa	aataaatctg	aaccaaactg	acaacatttc	1368											
catcctttca	gccactagct	tctgagccag	accagctgta	agctgaaacc	ccagcaagaa	1428											

gcaaggagag actgactgta ggcggccttg ggacatgtgc ttcttcccta agcgagaacc 1488  
ttagctgggg ccaatttgaa ggacccatgg gtggaatgtg ctgcctgtga gcttgtgggc 1548  
acagcaggac ccagcctggc tccttcttat gtccacggtg aatgtggttt cacaagacc 1608  
agagtataaa ctttcataga cattctcttt tagaaataat ccattaccct gtcttcaaaa 1668  
acaaaaaaaa aaaaaaagtg gtgttaaggt tttgaacatc acctagccaa gttagtaaaa 1728  
tctttatttg tatttcatct caattttttt aactattcat tttccttgta tgaattcttg 1788  
tgtgttttat gtgtaaatat attcattatt ttgacactat caatattctt tgtggttttg 1848  
taatttttac ttttattaat gactcaagct gtaaaaataa actaatttca acgtcgacgc 1908  
ggccgc 1914

<210> 6  
<211> 416  
<212> PRT  
<213> Mus musculus

<400> 6  
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
1 5 10 15  
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly  
20 25 30  
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu  
35 40 45  
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
50 55 60  
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe  
65 70 75 80  
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala  
85 90 95  
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala  
100 105 110  
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
115 120 125  
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
130 135 140  
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser  
145 150 155 160  
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser  
165 170 175

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr  
 180 185 190  
 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser  
 195 200 205  
 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Gln Pro  
 210 215 220  
 Arg Leu Arg His Cys Ala His Arg Ala Cys Cys Gln Tyr His Arg Asp  
 225 230 235 240  
 Ser Ala Pro Met Tyr Gly Pro Val His Leu Ile Pro Ser Leu Cys Cys  
 245 250 255  
 Glu Glu Ala Arg Ser Ser Ala Arg Ala Val Leu Gly Cys Gly Leu Arg  
 260 265 270  
 Ser Pro Thr Thr Leu Gln Glu Arg Asn Pro Ala Ser Val Gly Asp Thr  
 275 280 285  
 Met Pro Ala Phe Phe Gly Ser Val Ser Arg Ser Ile Cys Ala Glu Phe  
 290 295 300  
 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Leu Gly Gly Asp Ser Ser  
 305 310 315 320  
 Leu Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Thr Asn Ser Leu  
 325 330 335  
 Asn Pro Glu Asn Glu Ser Ala Ala Ser Leu Asp Ser Ser Gly Gly Gln  
 340 345 350  
 Asp Leu Ala Gly Thr Ala Ala Leu Glu Ser Ser Gly Asn Val Ser Glu  
 355 360 365  
 Ser Thr Asp Ser Pro Arg His Gly Asp Thr Gly Thr Val Trp Glu Gln  
 370 375 380  
 Thr Leu Ala Gln Asp Ala Gln Arg Thr Pro Ser Gln Gly Gly Trp Glu  
 385 390 395 400  
 Asp Arg Glu Asn Leu Asn Leu Ala Met Pro Thr Ala Phe Gln Asp Ala  
 405 410 415

<210> 7  
 <211> 27  
 <212> DNA  
 <213> Mus musculus

<400> 7  
 aggccatctt cctgacgtgg aggtgtg

<210> 8

